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# Spectral analysis for gene communities in cancer cells

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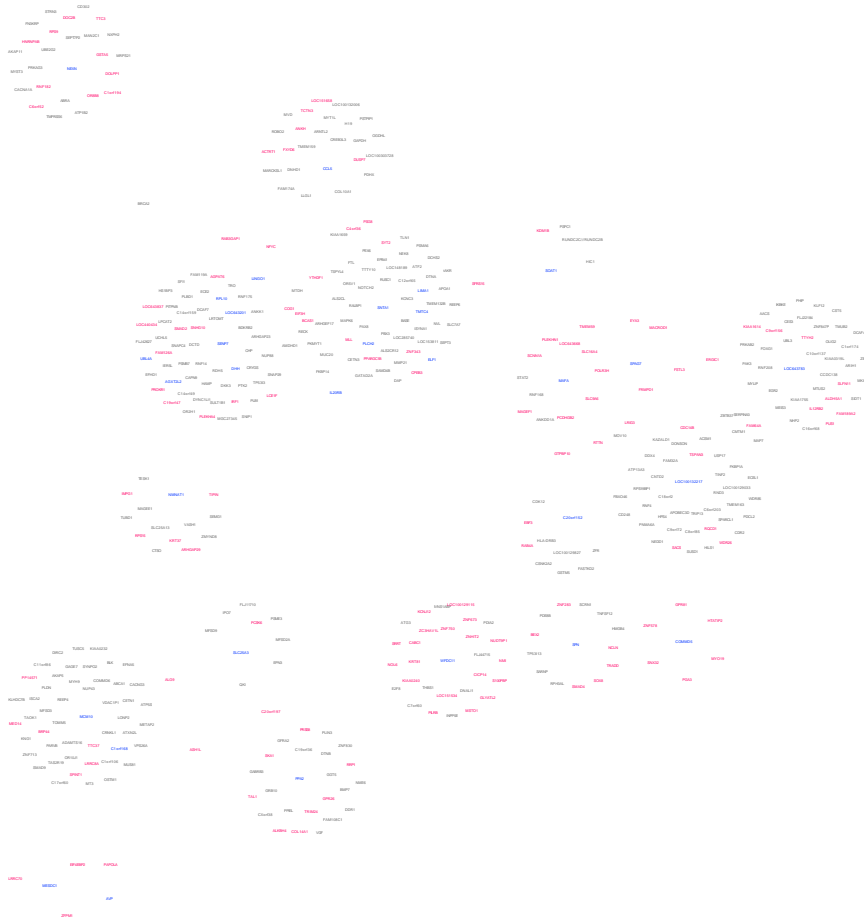
## Supplementary File

Title: Spectral analysis for gene communities in cancer cells

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Supplementary Figures 1-3 are deposited in the public website: “NDEx-The Network Data Exchange.” URL: <https://home.ndexbio.org/index/>

### Supplementary Figure 1



Supplementary Figure 1 caption:

A network graph for the sub-network of the gene interaction network in colon cancer. The extracted edges which have  $\Delta > 25$  are shown, where  $\Delta$  is the node degree discrepancy. The node attribute ‘Degree’ in this graph shows the node degree  $k$  in the original network before the extraction of the edges. Node sizes are proportional to  $k$  and node colors are dependent of  $k$ . The node labels are gene names and the label colors are purple for  $k=1$  node, red for nodes which have  $2 \leq k \leq 6$ , blue for nodes  $k \geq 25$ , and gray for  $6 < k < 25$  nodes.

DOI: **10.18119/N97S31**

### [Supplementary Figure 2](#)

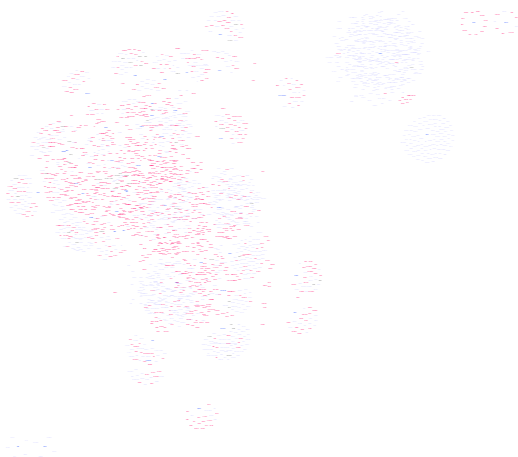


Supplementary Figure 2 caption:

A network graph for the sub-network of the gene interaction network in colorectal cancer (ID:125). The disassortative communities which have edges  $\Delta > 25$  are shown, where  $\Delta$  is the node degree discrepancy. The node color and the node size are the same as in Suppl. Fig. 1.

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### [Supplementary Figure 3](#)



Supplementary Figure 3 caption:

A network graph for the sub-network of the gene interaction network in breast cancer (ID:248). The disassortative communities which have edges  $\Delta > 25$  are shown, where  $\Delta$  is the node degree discrepancy. The node color and the node size are the same as in Suppl. Fig. 1.

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